

SEQUENCE LISTING

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<140> PCT/GB2004/005325

<141> 2004-12-20

<150> GB 0329684.5

<151> 2003-12-22

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<151> 2003-12-22

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Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe	50	55	60
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr	65	70	75
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Ala Ser Ile Ser Asp Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Asn Val	50	55	60	

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
65 70 75 80

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35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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35 40 45

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser
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Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
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35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
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Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
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Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile

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70

75

80

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<223> Murine gamma 2b constant region reverse primer

<400> 76

ggatcccggg agtggataga ctgatgg

27

<210> 77

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Murine kappa constant region reverse primer

<400> 77
ggatcccggg tggatggtgg gaagatg 27

<210> 78

<211> 52

<212> DNA

<213> Artificial sequence

<220>

<223> 2A10 VH forward primer

<400> 78
actcataagc ttgccaccat gggatggagc tgtatcatcc tctttttggt ag 52

<210> 79

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> VH reverse primer

<400> 79
actatgacta gtgtgccttg gccccagtag 30

<210> 80

<211> 42

<212> DNA

<213> Artificial sequence

<220>

<223> VL forward primer

<400> 80
actcataagc ttgccaccat gaggtgctct cttcagtttc tg 42

<210> 81

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> VL reverse primer

<400> 81

actatgcgta cgtttcagct ccagcttgg

29

<210> 82

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> CAMPATH-1H signal sequence

<400> 82

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser

<210> 83

<211> 120

<212> PRT

<213> Homo sapiens

<400> 83

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gln Trp Leu Val Ile Leu Asn Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 84

<211> 113

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VH construct H1

<400> 84

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Glu Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 100 105 110

Ser

<210> 85

<211> 112

<212> PRT

<213> Homo sapiens

<400> 85

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Gly Leu Val Tyr Ser
 20 25 30

Asp Gly Asp Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
 85 90 95

Thr His Trp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 86

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> Humanised VL construct L11

<400> 86

Asp Ile Val Ile Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
85 90 95

Val Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 87

<211> 201

<212> PRT

<213> Homo sapiens

<400> 87

Met	Gln	Glu	Ser	Leu	Tyr	Pro	Ala	Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu
1				5					10					15	
Glu	Ser	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu
			20					25					30		
Ala	Pro	Leu	Asn	Ser	Ala	Val	Pro	Ser	Ala	Gly	Ala	Ser	Val	Ile	Gln
		35					40					45			
Pro	Ser	Ser	Ser	Pro	Leu	Glu	Ala	Ser	Ser	Val	Asn	Tyr	Glu	Ser	Ile
	50					55					60				
Lys	His	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	Met	Ser	Val
65					70					75					80
Ser	Leu	Lys	Lys	Val	Ser	Gly	Ile	Lys	Glu	Glu	Ile	Lys	Glu	Pro	Glu
				85					90					95	
Asn	Ile	Asn	Ala	Ala	Leu	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile	Ser	Ile
		100						105					110		
Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Ala	Glu	Pro	Ala	Pro
		115					120					125			
Asp	Phe	Ser	Asp	Tyr	Ser	Glu	Met	Ala	Lys	Val	Glu	Gln	Pro	Val	Pro
	130					135					140				
Asp	His	Ser	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro	Asp	Ser	Glu	Pro	Val
145					150					155					160
Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Asp	Val	Pro	Gln	Lys	Gln	Asp
				165					170					175	
Glu	Thr	Val	Met	Leu	Val	Lys	Glu	Ser	Leu	Thr	Glu	Thr	Ser	Phe	Glu
			180					185					190		
Ser	Met	Ile	Glu	Tyr	Glu	Asn	Lys	Glu							
		195					200								

<210> 88

<211> 462

<212> PRT

<213> Artificial sequence

<220>

<223> anti-NOGO antibody heavy chain

<400> 88

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn
65 70 75 80

Glu Lys Phe Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Glu Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Leu Val
115 120 125

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
130 135 140

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 165 170 175

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 180 185 190

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 195 200 205

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 210 215 220

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 225 230 235 240

Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe
 245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly

385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 89

<211> 238

<212> PRT

<213> Artificial sequence

<220>

<223> anti-NOGO antibody light chain

<400> 89

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asp Ile Val Ile Thr Gln Ser Pro Leu Ser Leu Pro Val
20 25 30

Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu
35 40 45

Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro
50 55 60

Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
100 105 110

Gln Gln Leu Val Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 90

<211> 1428

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 88

<400> 90

aagctttaca gttactcagc acacaggacc tcaccatggg atggagctgt atcatcctct 60

tcttggtagc aacagctaca ggtgtccact cccaggtgca gctggtgcag tctggggctg 120

aggtgaagaa gcctggggcc tcagtgaagg tttcctgcaa ggcattctgga tacaccttca	180
ccagctactg gatgcactgg gtgcgacagg cccctggaca agggcttgag tggatgggaa	240
atattaatcc tagcaatggg ggtactaact acaatgagaa gttcaagagc agagtcacca	300
tgaccagggg cacgtccacg agcacagtct acatggagct gagcagcctg agatctgagg	360
acacggccgt gtattactgt gaactgggac agggctactg gggccagggg aactagtca	420
cagtctcttc agcctccacc aaggggccat cggctcttccc cctggcacc cctccaaga	480
gcacctctgg gggcacagcg gccctgggct gcctgggcaa ggactacttc cccgaaccgg	540
tgacgggtgc gtggaactca ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc	600
tacagtcttc aggactctac tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg	660
gcaccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag gtggacaaga	720
aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccc gcacctgaac	780
tcgcgggggc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc ctcattgatct	840
cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac cctgagggtca	900
agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag ccgcgggagg	960
agcagtacaa cagcacgtac cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc	1020
tgaatggcaa ggagtacaag tgcaagggtct ccaacaaagc cctcccagcc cccatcgaga	1080
aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc ctgcccccat	1140
cccgggatga gctgaccaag aaccagggtca gcctgacctg cctgggtcaaa ggcttctatc	1200
ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac tacaagacca	1260
cgcctcccgt gctggactcc gacggctcct tcttctctta cagcaagctc accgtggaca	1320
agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag gctctgcaca	1380
accactacac gcagaagagc ctctccctgt ctccgggtaa atgaattc	1428

<210> 91

<211> 758

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 89

<400> 91

```
aagctttaca gttactcagc acacaggacc tcaccatggg atggagctgt atcatcctct    60
tcttggtagc aacagctaca ggtgtccact ccgatattgt gataaaccag tctccactct    120
ccctgcccgt cacccttgga cagccggcct ccatctcctg caggtctagt aagagtctcc    180
tatataagga tgggaagaca tacttgaatt ggtttcagca gaggccaggc caatctccac    240
agctcctaat ttatttgatg tccacccgtg catctggggg cccagacaga ttcagcgggc    300
gtgggtcagg cactgatttc aactgaaaa tcagcagggt ggaggctgag gatgttgggg    360
tttattactg ccaacaactt gtagagtatc cgctcacgtt tggccagggg accaagctgg    420
agatcaaacg tacggtggct gcaccatctg tcttcatctt cccgccatct gatgagcagt    480
tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc agagaggcca    540
aagtacagtg gaaggtggac aacgccctcc aatcgggtaa ctcccaggag agtgtcacag    600
agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg agcaaagcag    660
actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg agctcgcccc    720
tcacaaagag cttcaacagg ggagagtgtt aggaattc                                758
```

<210> 92

<211> 462

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain sequence for HcLc

<400> 92

```
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1           5           10          15
```

```
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys
20          25          30
```

```
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35          40          45
```


Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn
 65 70 75 80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Glu Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Leu Val
 115 120 125

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 130 135 140

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 165 170 175

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 180 185 190

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 195 200 205

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 210 215 220

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 225 230 235 240

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 93

<211> 1405

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 92

<400> 93

aagcttgcca ccatgggatg gagctgtatc atcctctttt tggtagcagc agctacaggt	60
gtccactccc aggtccaact gcagcagcct gggactgaac tggatgaagcc tggggcttca	120
gtgaagctgt cctgcaaggc ttctggctac accttcacca gctactggat gcactgggtg	180
aagcagagggc ctggacaagg ccttgagtgg attggaaata ttaatcctag caatgggtgt	240
actaactaca atgagaagtt caagagcaag gccacactga ctgtagacaa atcctccagc	300
acagcctaca tgcagctcag cagcctgaca tctgaggact ctgcggtcta ttattgtgaa	360
ctgggacagg gctactgggg ccaaggcaca ctagtcacag tctcctcagc ctccaccaag	420
ggcccatcgg tcttccccct ggacacctcc tccaagagca cctctggggg cacagcggcc	480
ctgggctgcc tggatcaagg ctacttcccc gaaccggtga cgggtgctgt gaactcaggc	540
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc	600
ctcagcagcg tggatgacct gccctccagc agcttgggca ccagaccta catctgcaac	660
gtgaatcaca agcccagcaa caccaagggt gacaagaaag ttgagcccaa atcttgtgac	720
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc	780
ctcttcccc caaaacccaa ggacacctc atgatctccc ggacctctga ggtcacatgc	840
gtggtggtgg acgtgagcca cgaagacct gaggtcaagt tcaactggta cgtggacggc	900
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt	960
gtggtcagcg tcctcacctg cctgcaccag gactggctga atggcaagga gtacaagtgc	1020
aaggtctcca acaaagccct ccagccccc atcgagaaaa ccatctcca agccaaaggg	1080
cagccccgag aaccacaggt gtacacctg ccccatccc gggatgagct gaccaagaac	1140
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg	1200
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccggtgt ggactccgac	1260
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac	1320
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1380
tccctgtctc cgggtaaatg aattc	1405

<210> 94

<211> 239

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain sequence for HcLc

<400> 94

Met Arg Cys Ser Leu Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser
1 5 10 15

Gly Val Ser Gly Asp Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro
20 25 30

Val Thr Ser Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45

Leu Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg
50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala
65 70 75 80

Ser Gly Val Ser Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Glu Ile Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

Cys Gln Gln Leu Val Glu Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp

165

170

175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 95

<211> 738

<212> DNA

<213> Artificial sequence

<220>

<223> Polynucleotide encoding SEQ ID NO: 94

<400> 95

```

aagcttgcca ccatgagggtg ctctcttcag tttctggggg tgcttatgtt ctggatctct    60
ggagtcagtg gggatattgt gataaccag gatgaactct ccaatcctgt cacttctgga    120
gaatcagttt ccatctcctg caggtctagt aagagtctcc tatataagga tgggaagaca    180
tacttgaatt ggtttctgca gagaccagga caatctcctc agctcctgat ctatttgatg    240
tccacccgtg catcaggagt ctgagaccgg ttagtgaggca gtgggtcagg aacagatttc    300
accctggaaa tcagtagagt gaaggctgag gatgtgggtg tgtattactg tcaacaactt    360
gtagagtatc cgctcacgtt cggtgctggg accaagctgg agctgaaacg tacggtggct    420
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct    480
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggac    540
aacgccctcc aatcggttaa ctcccaggag agtgtcacag agcaggacag caaggacagc    600
acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc    660
tacgcctgcg aagtcaccca tcagggcctg agctcgcccc tcacaaagag cttcaacagg    720

```

ggagagtgtt aggaattc

738

<210> 96

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Motif

<400> 96

Tyr Glu Asn Pro
1

<210> 97

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Motif

<400> 97

Lys Lys Gln Asn
1